



#5

## SEQUENCE LISTING

<110> Medlock, Eugene  
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<120> IL-17 Like Molecules and Uses Thereof

<130> 01017/37128C

<140> 10/037,591

<141> 2001-12-21

<150> 09/886,404

<151> 2001-06-21

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<151> 2001-03-16

<150> 60/266,159

<151> 2001-02-02

<150> 60/213,125

<151> 2000-06-22

<160> 24

<170> PatentIn Ver. 2.0

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Met Tyr Gln Val Val Ala

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5

ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224

Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser  
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tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272

Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp  
25 30 35

agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320

Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His  
40 45 50

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc	368
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala	
55 60 65 70	
atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc	416
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro	
75 80 85	
cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta	464
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu	
90 95 100	
cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac	512
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr	
105 110 115	
cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc	560
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly	
120 125 130	
acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta	608
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu	
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 35 40 45  
 Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly  
 50 55 60  
 Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg  
 65 70 75 80  
 Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys  
 85 90 95  
 Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly  
 100 105 110  
 Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro  
 115 120 125  
 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg  
 130 135 140

Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met  
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<220>  
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 gtc agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc 96  
 Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys  
 20 25 30  
 ccc agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct 144  
 Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser  
 35 40 45  
 gca tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa 192  
 Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu  
 50 55 60  
 tcc tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct 240  
 Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser  
 65 70 75 80  
 cct tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac 288  
 Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp  
 85 90 95  
 ctg tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca 336  
 Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr  
 100 105 110  
 ggc tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac 384  
 Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn  
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 Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His  
 130 135 140  
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 Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys  
 145 150 155 160  
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 Val Cys Val Arg Pro Arg Val Met Ala  
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 <213> Mus musculus

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 Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser  
 35 40 45  
 Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu  
 50 55 60  
 Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser  
 65 70 75 80  
 Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp  
 85 90 95  
 Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr  
 100 105 110  
 Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn  
 115 120 125  
 Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His  
 130 135 140  
 Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys  
 145 150 155 160  
 Val Cys Val Arg Pro Arg Val Met Ala  
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 <212> PRT  
 <213> Homo sapiens

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 Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn  
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 Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser  
                     50                    55                    60  
 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu  
                     65                    70                    75                    80  
 Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His  
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 Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser  
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 Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His  
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 Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys  
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 Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys  
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 Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg  
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 Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val  
                     50                    55                    60  
 Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val  
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 Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg  
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 Cys Thr Cys Ile Phe  
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<213> Homo sapiens

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Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg  
35 40 45

Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val  
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val  
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg  
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Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly  
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Cys Thr Cys Ile Phe  
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<210> 8

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<212> PRT

<213> Homo sapiens

<400> 8

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Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser His Gly  
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Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly Gln Ala Pro  
35 40 45

Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val  
50 55 60

Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu  
65 70 75 80

Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val  
85 90 95

Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg  
100 105 110

Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu  
115 120 125

Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala  
130 135 140

Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg  
 145 150 155 160

Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe  
 165 170 175

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<220>  
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 <222> (511)..(987)

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 Met Ile Val Gly Thr His Thr Val  
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agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc ccc 582  
 Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys Pro  
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agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct gca 630  
 Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser Ala  
 25 30 35 40

tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa tcc 678  
 Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu Ser  
 45 50 55

tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct cct 726  
 Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser Pro  
 60 65 70

tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac ctg 774  
 Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp Leu  
 75 80 85

tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca ggc 822  
 Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly  
 90 95 100

tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac cag 870  
 Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn Gln  
 105 110 115 120

acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat cgc 918  
 Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His Arg  
 125 130 135

cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt gtg 966  
 Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys Val  
 140 145 150

tgt gtg cgg ccc cgg gtc atg gcttagtcat gctcaccacc tgcctgaggc 1017  
 Cys Val Arg Pro Arg Val Met  
 155

tgatgccccg ttgggagaga gggccaggtg tacaatcacc ttgccaatgc gggccggggtt 1077  
 caagccctcc aaagccctac ctgaagcagc aggctcccg gacaagatgg aggacttggg 1137  
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 <212> PRT  
 <213> Mus musculus

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Glu Trp Leu Lys Trp Ser Ser Ala Ser Val Ser Pro Pro Glu Pro Leu  
 35 40 45

Ser His Thr His His Ala Glu Ser Cys Arg Ala Ser Lys Asp Gly Pro  
 50 55 60

Leu Asn Ser Arg Ala Ile Ser Pro Trp Ser Tyr Glu Leu Asp Arg Asp  
 65 70 75 80

Leu Asn Arg Val Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro  
 85 90 95



His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Leu Gly Asn  
 100 105 110

Ser Val Pro Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys  
 115 120 125

His Gly Glu Glu Gly Thr His Arg Arg Tyr Cys Leu Glu Arg Arg Leu  
 130 135 140

Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met  
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<210> 11  
 <211> 27  
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<220>  
 <223> Description of Artificial Sequence: Epogen signal  
 peptide

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Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly  
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<210> 12  
 <211> 233  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: peptide of Fc  
 fragment

<400> 12  
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 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
 115 120 125  
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
 130 135 140  
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
 145 150 155 160  
 Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 165 170 175  
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 180 185 190  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 195 200 205  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 210 215 220  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230

<210> 13  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Peptide of HIV  
 TAT protein

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 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
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<210> 14  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Peptide of HIV  
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Arg Arg Arg

<210> 15  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer

<400> 15  
tagggccagt gaagatgg 18

<210> 16  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

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<210> 17  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (50)..(1555)

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Met Ser Leu  
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Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu  
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154  
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met  
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202  
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu  
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250  
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn  
55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298  
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala  
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346  
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys  
85 90 95

gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct 394  
Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser  
100 105 110 115

ggg ggt aaa tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac 442  
Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn  
120 125 130

aca gtc tat ttc att ggg gcc cat aat att cct aat gca aat atg aat	490
Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn	
135 140 145	
gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta	538
Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu	
150 155 160	
gac cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg	586
Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu	
165 170 175	
tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa	634
Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu	
180 185 190 195	
gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc	682
Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile	
200 205 210	
caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag	730
Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln	
215 220 225	
aag aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt	778
Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser	
230 235 240	
gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc	826
Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser	
245 250 255	
gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc cca caa aca ggc	874
Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly	
260 265 270 275	
gtc cct ttc cct ctg gat aac aac aaa agc aag ccg gga ggc tgg ctg	922
Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu	
280 285 290	
cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg gtg ctg gtg gca	970
Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala	
295 300 305	
ggg atc tat cta atg tgg agg cac gaa agg atc aag aag act tcc ttt	1018
Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe	
310 315 320	
tct acc acc aca cta ctg ccc ccc att aag gtt ctt gtg gtt tac cca	1066
Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro	
325 330 335	
tct gaa ata tgt ttc cat cac aca att tgt tac ttc act gaa ttt ctt	1114
Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu	
340 345 350 355	
caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag	1162
Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys	
360 365 370	

aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc act caa aag aag 1210  
 Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys  
 375 380 385

gca gca gac aaa gtc gtc ttc ctt tcc aat gac gtc aac agt gtg 1258  
 Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val  
 390 395 400

tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc agt gag aac tct 1306  
 Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser  
 405 410 415

caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc agt gat cta aga 1354  
 Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg  
 420 425 430 435

agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402  
 Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile  
 440 445 450

gat aca aaa gac gat tac aat gct ctc agt gtc tgc ccc aag tac cac 1450  
 Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His  
 455 460 465

ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498  
 Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys  
 470 475 480

cag cag gtg tca gca gga aaa aga tca caa gcc tgc cac gat ggc tgc 1546  
 Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys  
 485 490 495

tgc tcc ttg tagccacccc atgagaagca agagacctta aaggcttcct 1595  
 Cys Ser Leu  
 500

atccccaccaa ttacagggaa aaaacgtgtg atgatacctga agcttactat gcagcctaca 1655

aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaataatt gctaactaat 1715

gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt tatacataga 1775

aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca ataaagcatc 1835

ttcagc 1841

<210> 18  
 <211> 502  
 <212> PRT  
 <213> Homo sapiens

<400> 18.  
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
 20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 65 70 75 80  
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 85 90 95  
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr  
 100 105 110  
 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val  
 115 120 125  
 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala  
 130 135 140  
 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro  
 145 150 155 160  
 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala  
 165 170 175  
 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu  
 180 185 190  
 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met  
 195 200 205  
 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu  
 210 215 220  
 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr  
 225 230 235 240  
 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr  
 245 250 255  
 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro  
 260 265 270  
 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly  
 275 280 285  
 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val  
 290 295 300  
 Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys  
 305 310 315 320  
 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val  
 325 330 335  
 Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr  
 340 345 350  
 Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp  
 355 360 365

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr  
 370 375 380  
 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val  
 385 390 395 400  
 Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser  
 405 410 415  
 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser  
 420 425 430  
 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe  
 435 440 445  
 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro  
 450 455 460  
 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu  
 465 470 475 480  
 His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His  
 485 490 495  
 Asp Gly Cys Cys Ser Leu  
 500

<210> 19  
 <211> 2015  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (50)..(1729)

<400> 19  
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 Met Ser Leu  
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gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106  
 Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu  
 5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154  
 Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met  
 20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202  
 Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu  
 40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250  
 Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn  
 55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298  
 Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala  
 70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt	346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys	
85 90 95	
gtg agg ctg gag tgc agt ggt gcg atc atg gct cgc tgc gac ctc aat	394
Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys Asp Leu Asn	
100 105 110 115	
ctt ctg ggc tca agc gat cgt tct gct tca gcc tcc cga gcg gct ggg	442
Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg Ala Ala Gly	
120 125 130	
act gca ggc gtg ggc cac cag acc tgg cta att ttt gta gtt ttt gta	490
Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val Val Phe Val	
135 140 145	
gag ggg ggt ttc acc gtg ttg ctg gtc ttg aat tcc agt gct cag gcg	538
Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser Ala Gln Ala	
150 155 160	
atc tgc ctg cct cgg ctt ccc aaa gtg ctg gga tta cag tgg aca ttt	586
Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln Trp Thr Phe	
165 170 175	
tcc tac atc ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg	634
Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly	
180 185 190 195	
gcc cat aat att cct aat gca aat atg aat gaa gat ggc cct tcc atg	682
Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met	
200 205 210	
tct gtg aat ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat	730
Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr	
215 220 225	
aaa aaa aag tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act	778
Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr	
230 235 240	
gct tgt aag aag aat gag gag aca gta gaa gtg aac ttc aca acc act	826
Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr	
245 250 255	
ccc ctg gga aac aga tac atg gct ctt atc caa cac agc act atc atc	874
Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile	
260 265 270 275	
ggg ttt tct cag gtg ttt gag cca cac cag aag aaa caa acg cga gct	922
Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala	
280 285 290	
tca gtg gtg att cca gtg act ggg gat agt gaa ggt gct acg gtg cag	970
Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln	
295 300 305	
ctg act cca tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa	1018
Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys	
310 315 320	
gga aca gtt gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat	1066
Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp	
325 330 335	



aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct	1114
Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser	
340 345 350 355	
ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg	1162
Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp	
360 365 370	
agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg	1210
Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu	
375 380 385	
ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat	1258
Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His	
390 395 400	
cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt	1306
His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser	
405 410 415	
gag gtc atc ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt	1354
Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly	
420 425 430 435	
cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc	1402
Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val	
440 445 450	
ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc	1450
Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly	
455 460 465	
aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt	1498
Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu	
470 475 480	
gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac	1546
Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His	
485 490 495	
aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac	1594
Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr	
500 505 510 515	
aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act	1642
Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr	
520 525 530	
gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga	1690
Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly	
535 540 545	
aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccccc	1739
Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu	
550 555 560	
atgagaagca agagacctta aaggcttccct atccccaccaa ttacagggaa aaaacgtgtg	1799
atgatcctga agcttactat gcagcctaca aacagcctta gtaattaaaa catttttatac	1859
caataaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat	1919

ttacaacttc aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta 1979  
accattttga taatgcaaca ataaagcatc ttcagc 2015

<210> 20  
<211> 560  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
1 5 10 15  
Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
20 25 30  
Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
35 40 45  
Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
50 55 60  
Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
65 70 75 80  
Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
85 90 95  
Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys  
100 105 110  
Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg  
115 120 125  
Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val  
130 135 140  
Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser  
145 150 155 160  
Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln  
165 170 175  
Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr  
180 185 190  
Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly  
195 200 205  
Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile  
210 215 220  
Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro  
225 230 235 240  
Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe  
245 250 255  
Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser  
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln  
 275 280 285  
 Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala  
 290 295 300  
 Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile  
 305 310 315 320  
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe  
 325 330 335  
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu  
 340 345 350  
 Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr  
 355 360 365  
 Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr  
 370 375 380  
 Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile  
 385 390 395 400  
 Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His  
 405 410 415  
 Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala  
 420 425 430  
 Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp  
 435 440 445  
 Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly  
 450 455 460  
 Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu  
 465 470 475 480  
 Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile  
 485 490 495  
 His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys  
 500 505 510  
 Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys  
 515 520 525  
 Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val  
 530 535 540  
 Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu  
 545 550 555 560

<210> 21  
 <211> 521  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
 20 25 30  
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
 35 40 45  
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 65 70 75 80  
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 85 90 95  
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser  
 100 105 110  
 Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn  
 115 120 125  
 Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn  
 130 135 140  
 Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu  
 145 150 155 160  
 Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu  
 165 170 175  
 Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu  
 180 185 190  
 Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile  
 195 200 205  
 Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln  
 210 215 220  
 Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser  
 225 230 235 240  
 Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser  
 245 250 255  
 Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly  
 260 265 270  
 Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu  
 275 280 285  
 Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 290 295 300  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 305 310 315 320  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 325 330 335  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 340 345 350

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 355 360 365  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 370 375 380  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 385 390 395 400  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 405 410 415  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 420 425 430  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 435 440 445  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 450 455 460  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 465 470 475 480  
 Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 485 490 495  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 500 505 510  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 515 520

<210> 22  
 <211> 585  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
 1 5 10 15  
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
 20 25 30  
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
 35 40 45  
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 65 70 75 80  
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 85 90 95  
 Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys  
 100 105 110  
 Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg  
 115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val  
 130 135 140  
 Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser  
 145 150 155 160  
 Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln  
 165 170 175  
 Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr  
 180 185 190  
 Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly  
 195 200 205  
 Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile  
 210 215 220  
 Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro  
 225 230 235 240  
 Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe  
 245 250 255  
 Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser  
 260 265 270  
 Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln  
 275 280 285  
 Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala  
 290 295 300  
 Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile  
 305 310 315 320  
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe  
 325 330 335  
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala  
 340 345 350  
 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 355 360 365  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 370 375 380  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 385 390 395 400  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 405 410 415  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 420 425 430  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 435 440 445  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
580 585

<210> 23  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 23  
gtacagtggc tgaccactca gaag

24

<210> 24  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Primer

<400> 24  
ggtggactac aagggtgaac agc

23